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RESULT 12
ENRN_BPT3
TD
    ENRN_BPT3
                             Reviewed;
    P20314;
AC
     01-FEB-1991, integrated into {\tt UniProtKB/Swiss-Prot.}
DT
DT
     01-FEB-1991, sequence version 1.
\mathsf{DT}
     25-NOV-2008, entry version 38.
    RecName: Full=Endodeoxyribonuclease 1;
DF.
DE
              EC=3.1.21.2;
DE
     AltName: Full=Endodeoxyribonuclease I;
DE
              Short=Endonuclease;
GN
    Name=3:
OS
    Enterobacteria phage T3 (Bacteriophage T3).
OC
     Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
     Autographivirinae; T7-like viruses.
OC
\circ x
    NCBI_TaxID=10759;
ОН
     NCBI_TaxID=562; Escherichia coli.
RN
     [1]
RP
    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC
     STRAIN=Luria;
     MEDLINE=90133923; PubMed=2614843; DOI=10.1016/0022-2836(89)90102-2;
RX
RA
     Beck P.J., Gonzalez S., Ward C.L., Molineux I.J.;
     "Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.";
RT
    J. Mol. Biol. 210:687-701(1989).
RL
CC
     -!- FUNCTION: Endodeoxyribonuclease I, which is expressed in the late
CC
         stage, is necessary for T3 genetic recombination and the breakdown
CC
         of host DNA. In the early stage of infection, T3 DNA replicates as
CC
         a linear monomer. In the late stage, the T3 DNA replicates via
CC
         linear concatemers several genomes in length. The gene 3 product
CC
         has also been implicated in the maturation of these concatemers.
CC
     -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC
       phosphooligonucleotide end-products.
CC
CC
     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC
     Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR
    EMBL; X17255; CAA35132.1; -; Genomic_DNA.
DR
     PIR; S07505; S07505.
     RefSeq; NP_523312.1;
DR
    HSSP; P00641; 1M0D.
SMR; P20314; 17-145.
DR
DR
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DR
DR
     GO; GO:0005634; C:nucleus; IEA:InterPro.
    GO; GO:0008833; F:deoxyribonuclease IV (phage-T4-induced) act. . .; IEA:InterPro.
DR
DR
     GO; GO:0003677; F:DNA binding; IEA:InterPro.
     GO; GO:0015074; P:DNA integration; IEA:InterPro.
DR
     GO; GO:0016032; P:viral reproduction; IEA:InterPro.
DR
DR
     InterPro; IPR008029; Endonuclease-I_phage.
DR
     InterPro; IPR011578; Restrict_endonuc_C/endonuc_I.
     Gene3D; G3DSA:3.40.91.30; Restrict_endonuc_C/endonuc_I; 1.
DR
     Pfam; PF05367; Phage_endo_I; 1.
     4: Predicted;
PE
KW
    Endonuclease; Hydrolase; Nuclease.
FT
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                      152
FΤ
                                  /FTId=PRO_0000106485.
    SEQUENCE 152 AA; 17432 MW; BFCDE82A4C0D611B CRC64;
SO
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                                                                  0; Gaps
Ov
            1 MAGYSAKGIRKVGAFRSGLEDKVSKQLESKGIKFEYEEWKVPYVIPASNHTYTPDFLLPN 60
              1 MAGAYAARCTQGRAFRSGLEDKVSKQLESKGIKFDYELWRIPYVIPESDHLYTPDFLLPN 60
Db
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Qу
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Qу
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Db
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10/585964 SEQ ID NO:25
RESULT 12
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     RefSeq; NP_523312.1;
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     HSSP; P00641; 1M0D.
DR
     SMR; P20314; 17-145.
DR
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DR
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DR
     Gene3D; G3DSA:3.40.91.30; Restrict_endonuc_C/endonuc_I; 1.
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     Pfam; PF05367; Phage_endo_I; 1.
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     4: Predicted:
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FΤ
                       152 Endodeoxyribonuclease 1.
FT
                                    /FTId=PRO_0000106485.
     SEQUENCE 152 AA; 17432 MW; BFCDE82A4C0D611B CRC64;
SO
 Query Match 77.7%; Score 615; DB 1; Length 152; Best Local Similarity 83.1%; Pred. No. 5.6e-49; Matches 113; Conservative 11; Mismatches 12; Indels 0; Gaps
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Db	14 AFRSGLEDKVSKQLESKGIKFDYELWRIPYVIPESDHLYTPDFLLPNGIFIETKGLWDSD 73
Qу	74 DRKKHLLIREQHPELDIRIVFSSSRTKLYKGSPTSYGEFCEKHGIKFADKLIPAEWIKEP 133
Db	74 DRKKHLLIREQHPELDIRLVFSSSRSKLYKGSPTSYGEWCEKHGILFADKLIPVAGVKEP 133
Qy	134 KKEVSFDRLKRKGGKK 149
Db	134 KKEVPFDKFKTKKGVK 149